

- 56 -

ATGTTTCGGCTCCGCCCCCAGCGTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTG
TTGTGGAAGCTCGCGGGGTGCTGCGGGAGTCCGGGGATGTGGTCCTGTCTGGCTGTAGC
ACCTTGAGCCTGCTGACTCCCACACTGCAACAGCTGAACCACGTATTTGAGCTGCACCTG
GGGCCATGGGGCCCTGGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCCTGCCGACTCC
CCTGTTATTCTTCAGCTTCAGTTTCTCTTCGATGTGCTGCAGAAAACACTTTCACCTCAAG
CTGGTCCATGTTGCTGGTCTGCGCCCCACAGGGCCCATCAAGATTTTCCCCTCAAATCC
CTTCGGCACCTGGAGCTCCGAGGTGTTCCCCTCCACTGTCTGCATGGCCTCCGAGGCATC
TACTCCCAGCTGGAGACCCTGATTTGCAGCAGGAGCCTCCAGGCATTAGAGGAGCTCCTC
TCAGCCTGCGGCGGCGACTTCTGCTCTGCCCTCCCTTGGCTGGCTCTGCTTTCTGCCAAC
TTCAGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTTGTCAGCTCTGCGT
TTCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTGAGGATTCCTGATGGATTGTGT
GAGCTCCACCATCTGGACATCTCCTATAATCGCCTGCATTGGTGCCAAGAATGGGACCC
TCAGGGGCTGCTCTGGGGTCTGATACTGCGAGGCAATGAGCTTCGGAGCCTGCATGGC
CTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTGGCATAAACCTGCTGGAAGGACAC
CGGGAGCTGTCACCACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTGGAGGGGAAC
CCTCTTTGGTTCCACCCTGAGCACCGAGCAGCCACTGCCAGTACTTGTACCCCGGGCC
AGGGATGCTGCTACTGGCTTCCTTCTCGATGGCAAGGTCTTGTCAGTACAGATTTTCAG
ACTCACACATCCTTGGGGCTCAGCCCCATGGGGCCACCTTTGCCCTGGCCAGTGGGGAGT
ACTCCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCCTCTCCTCAGGGGGTGTGTG
ACCCAGCCCCTGCTTCATAAGGTTAAGAGCCGAGTCCGTGTGAGCGGGCAAGCATCTCT
GAACCCAGTGATACGGACCCGGAGCCCCGAACCTCTGAACCCCTCTCCGGCTGGATGGTTC
GTGCAGCAGCACCCGGAGCTGGAGCTCATGAGCAGCTTCGGGAACGGTTCGGCCGCAAC
TGGCTGCAGTACAGGAGTCACCTGGAGCCCTCCGGAAACCTCTGCCGGCCACCCCACT

Figure 1A

- 57 -

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ACTTCTGCACCCAGTGCACCTCCAGCCAGCTCCCAGGGCCCCGACACTGCACCCAGACCT
TCACCCCCGCAGGAGGAAGCCAGAGGCCCCAGGAGTCACCACAGAAAATGTCAGAGGAG
GTCAGGGCGGAGCCACAGGAGGAGGAAGAGGAGAAGGAGGGGAAGGAGGAGAAGGAGGAG
5 GGGGAGATGGTGAACAGGGAGAAGAGGAGGCAGGAGAGGAGGAAGAAGAGGAGCAGGAC
CAGAAGGAAGTGAAGCGGAACCTCTGTCGCCCCCTTGTGGTGTGTCCCCCTGGAGGGCCT
GAGGGCATACGGGGCAGGGAATGCTTCTCAGGGTCACTTCTGCCCACCTGTTTGAGGTG
GAACTCCAAGCAGCTCGCACCTTGGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAG
ATAGAGCCGGAGGCCAGGCCAGAGGTGCGCCAGGCCACGGGCTCAGATCTGCTCCCT
GGAGCCCCCATCTCAGTCTGCGCTTCTCCTACATCTGCCCTGACCGGCAGTTGCGTCGC
TATTTGGTGCTGGAGCCTGATGCCACGCAGCTGTCCAGGAGCTGCTTGCCGTGTTGACC
CCAGTCACCAATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGGACCTCCTGCTGGGTAGA
TTCCAGTGTCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC
AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGGGAGCGGAAACAGGGAGAGCAGT
CTCTGGCTCCTTCTCCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACC
TTGACAGGGCCAAGAACAGCCACCTCAGGCACCGAGCACCCGTGACCATGGTAGTTGGA
GCCTCAGTCCCCCCCCCTGAGCGCTGTGGCCTCCGCTCTGTGGACCACCGACTCCGGCTCT
TCCTGGATGTTGAGGTGTTTACGCGATGCCAGGAGGAGTTCCAGTGCTGCCTCAAGGTGC
CAGTGGCATTGGCAGGCCACACTGGGGAGTTCATGTGCCTTGTGGTTGTGTCTGACCGCA
GGCTGTACCTGTTGA

Figure 1B.

ATGTTTCGGCTCCGCCCCCAGCGTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTG
TTGTGGAAGCTCGCGGGGTGCTGCGGGAGTCCGGGGATGTGGTCCTGTCTGGCTGTAGC
ACCCGTGAGCCTGTGACTCCCACACTGCAACAGCTGAACCACGTATTTGAGCTGCACCTG
5 GGGCCATGGGGCCCTGGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCCTGCCGACTCC
CCTGTTATTCTTCAGCTTCAGTTTCTCTTCGATGTGCTGCAGAAAACACTTTCACCTCAAG
CTGGTCCATGTTGCTGGTCTCGGCCACAGGGCCCATCAAGATTTTCCCCTCAAATCC
CTTCGGCACCTGGAGCTCCGAGGTGTTCCCCTCCACTGTCTGCATGGCCTCCGAGGCATC
TACTCCCAGCTGGAGACCCTGATTTGCAGCAGGAGCCTCCAGGCATTAGAGGAGCTCCTC
10 TCAGCCTGCGGCGGCGACTTCTGCTCTGCCCTCCCTTGGCTGGCTCTGCTTTCTGCCAAC
TTCAGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTTGTCAGCTCTGCGT
TTCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTCAGGGATTCCTGATGGATTTGTGT
GAGCTCCACCATCTGGACATCTCCTATAATCGCCTGCATTTGGTGCCAAGAATGGGACCC
TCAGGGGCTGCTCTGGGGGTCTGATACTGCGAGGCAATGAGCTTCGGAGCCTGCATGGC
CTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTGGCATAACAACCTGCTGGAAGGACAC
CGGGAGCTGTCACCACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTGGAGGGGAAC
CCTCTTTGGTTCCACCCTGAGCACCGAGCAGCCACTGCCAGTACTTGTACCCCGGGCC
AGGGATGCTGCTACTGGCTTCCTTCTCGATGGCAAGGTCTTGTCAGTACAGATTTTCAG
ACTCACACATCCTTGGGGCTCAGCCCCATGGGCCACCTTTGCCCTGGCCAGTGGGGAGT
20 ACTCCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCCTCTCCTCAGGGGGTGTGTG
ACCCAGCCCCTGCTTCATAAGGTTAAGAGCCGAGTCCGTGTGAGGCGGGCAAGCATCTCT
GAACCCAGTGATACGACCCGGAGCCCCGAACCTCTGAACCCCTCTCCGGCTGGATGGTTC
GTGCAGCAGCACCCGGAGCTGGAGCTCATGAGCAGCTTCCGGGAACGGTTCGGCCGCAAC

Figure 2A

- 59 -

5
10
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20
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TGGCTGCAGTACAGGAGTACCTGGAGCCCTCCGAAACCCTCTGCCGGCCACCCCACT
ACTTCTGCACCCAGTGCACCTCCAGCCAGCTCCCAGGGCCCCGACACTGCACCCAGACCT
TCACCCCGCAGGAGGAAGCCAGAGGCCCCAGGAGTACCACAGAAAATGTCAGAGGAG
GTCAGGGCGGAGCCACAGGAGGAGGAAGAGGAGAAGGAGGGGAAGGAGGAGAAGGAGGAG
GGGGAGATGGTGGAAACAGGGAGAAGAGGAGGCAGGAGAGGAGGAAGAAGAGGAGCAGGAC
CAGAAGGAAGTGGAAAGCGAACTCTGTCGCCCCCTTGTGGTGTGTCCCCTGGAGGGGCCT
GAGGGCGTACGGGGCAGGGAATGCTTCTCAGGGTCACTTCTGCCACCTGTTTGAGGTG
GAACTCCAAGCAGCTCGCACCTTGGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAG
ATAGAGCCGGAGGCCCAGGCCCAGAGGTGCGCCAGGCCACGGGCTCAGATCTGCTCCCT
GGAGCCCCATCCTCAGTCTGCGCTTCTCCTACATCTGCCCTGACCGGCAGTTGCGTCGC
TATTTGGTGCTGGAGCCTGATGCCCCACGCAGCTGTCCAGGAGCTGCTTGCCGTGTTGACC
CCAGTCACCAATGTGGCTCGGGAACAGCTTGGGGAGGCCAGGGACCTCCTGCTGGGTAGA
TTCCAGTGTCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCAGGATGGGATTAGAC
AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGAATCTCCTGCTGTGTGTCCTAAC
TGTGGTAGTGACCACGTGGTTCTCCTCGCTGTGTCTCGGGGAACCCCCAACAGGGAGCGG
AAACAGGGAGAGCAGTCTCTGGCTCCTTCTCCGTTTGCCAGCCCTGTCTGCCACCTCCT
GGCCATGGTGACCACCTTGACAGGGCCAAGAACAGCCCACCTCAGGCACCGAGCACCCGT
GACCATGGTAGTTGGAGCCTCAGTCCCCCCCCTGAGCGCTGTGGCCTCCGCTCTGTGGAC
CACCGACTCCGGCTCTTCTGGATGTTGAGGTGTTTCAAGCATGCCCAGGAGGAGTTCCAG
TGCTGCCTCAAGGTGCCAGTGGCATTTGGCAGGCCACACTGGGGAGTTTATGTGCCTTGTG
GTTGTGTCTGACCGCAGGCTGTACCTGTTGAAGGTGACTGGGGAGATGCGTGAGCCTCCA
GCTAGCTGGCTGCAGCTGACCCTGGCTGTTCCCCTGCAGGATCTGAGTGGCATAGAGCTG

Figure 2B

GGCCTGGCAGGCCAGAGCCTGCGGCTAGAGTGGGCAGCTGGGGCGGGCCGCTGTGTGCTG
CTGCCCCGAGATGCCAGGCATTGCCGGGCCTTCCTAGAGGAGCTCCTTGATGTCTTGCAG
TCTCTGCCCCCTGCCTGGAGGAAGTGTGTCTAGTGCCACAGAGGAGGAGGTCACCCCCAG
CACCGGCTCTGGCCATTGCTGGAAAAAGACTCATCCTTGAGGGCTCGCCAGTTCCTTCTAC
CTTCGGGCGTTCTCTGGTTGAAGGCCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCG
TCCACCCTGTTCTCTGTTAGATGAGGATGCTGCAGGGTCCCCGGCAGAGCCCTCTCCTCCA
GCAGCATCTGGCGAAGCCTCTGAGAAGGTGCCTCCCTCGGGGCGGGGCCCTGCTGTGCGT
GTCAGGGAGCAGCAGCCACTCAGCAGCCTGAGCTCCGTGCTGCTCTACCGCTCAGCCCCT
GAGGACTTGCGGCTGCTCTTCTACGATGAGGTGTCCCGGCTGGAGAGCTTTTGGGCACTC
CGTGTGGTGTGTCTCAGGAGCAGCTGACAGCCCTGCTTGCCTGGATCCGGGAACCATGGGAG
GAGCTGTTTTCCATCGGACTCCGGACAGTGATCCAAGAGGCGCTGGCCCTTGACCGATGA

Figure 2C.

- 61 -

MFGSAPQRPVAMTTAQRDSSLWKLGLLRESGDVVLSCSTLSLLTPTLQQLNHVFELHL
 GPWGPQTGFVALPSHPADSPVILQLQLFDVLQKTLCLKLVHVAGPGPTGPIKIFPFKS
 LRHLELRGVPLHLHGLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSAN
 FSYNALTALDSSLRLLSALRFLNLSHNQVQDCQGFMDLCELHHLDISYNRLHLVPRMGP
 5 SGALGVLIIRGNELRSLHGLEQLRNLRLHLDLAYNLLEGHRELSPLWLLAELRKLYLEGN
 PLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSTDFQHTSLGLSPMGPPPLPWPVGS
 TPETSGGPDLSDSLSSGGVVTQPLLHKVKSRVRVRRASISEPSDTPPEPRTLNPSPAGWF
 VQQHPELELMSSFRERFGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRP
 SPPQEEARGPQESPQKMSEEVRAEPQEEEEKEGKEEKEEGEMVEQGEEEEAGEEEEEEQD
 10 QKEVEAELCRPLLVCPLLEGPEGIRGECFLRVTSAPHLFEVELQAARTLERLELQSLEAAE
 IEPEAQQRSPRPTGSDLLPGAPILSLRFSYICPDRQLRRYLVLLEPDAAHAQVQELLAVLT
 PVTNVAREQLGEARDLLLGRFQCLRCGHEFKPEEPRMGLDSEEGWRPLFQKTGSCNRESS
 LWLLLRLPALSATLLAMVTTLTGPRTAHLRHRAPVTMVVGASVPPLSAVASALWTTDSGS
 SWMLRCSAMPRSSSAASRCQWHWQATLGSSCALWLCLTAGCTC

Figure 3.

- 62 -

MFGSAPQRPVAMTTAQRDSSLWKLGLLRESGDVVLSCSTLSLLTPTLQQLNHVFELHL
 GPWGPQGTGFVALPSHPADSPVILQLQFLFDVLQKTLCLKLVHVAGPGPTGPIKIFPFKS
 LRHLELRGVPLHCLHGLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSAN
 FSYNALTALDSSLRLLSALRFLNLSHNQVQDCQGFMDLCELHHLDISYNRLHLVPRMGP
 5 SGAALGVLIIRGNELRSLHGLEQLRNLRLHLDLAYNLLEGHRELSPLWLLAELRKLYLEG
 PLWFHPEHRAATAQYLSRPARDAATGFLLDGKVLSTDFQHTSLGLSPMGPPLPWPVGS
 TPETSGGPDLSDSLSSGGVVTQPLLHKVKSRRVRRASISEPSDTPPEPRTLNPSPAGWF
 VQOHPPELMSFRFRGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRP
 SPPQEEARGPQESPQKMSEEVRAEPQEEEEKEGKEEKEEGEMVEQEEEAGEEEEEEQD
 QKEVEAELCRPLLVCPLGPEGVRGECFLRVTSAPHLFEVELQAARTLERLELQSLEAAE
 IEPEAQQRSPRPTGSDLLPGAPILSLRFSYICPDRQLRRYLVLLEPDAAVQELLAVLT
 PVTNVAREQLGEARDLLLGRFQCLRCGHEFKPEEPRMGLDSEEGWRPLFQKTESPAVCPN
 CGSDHVLLAVSRGTPNRERKQGEQSLAPSPFASPVCHPPGHGDHLDRAKNSPPQAPSTR
 DHGWSLSPPPERCGLRSVDHRLRLFLDVEVFSDAQEEFQCCLKVPVALAGHTGEFMCLV
 VVSDRRLYLLKVTGEMREPPASWLQTLAVPLQDLSGIELGLAGQSLRLEWAAGAGRCVL
 LPRDARHCRAFLEELLDVLQSLPPAWRNCVSATEEEVTPQHRLWPLLEKDSSLEARQFFY
 LRAFLVEGPSTCLVSLLLTPSTLFLLEDAAGSPAEPSPPAASGEASEKVPPSGPGPAVR
 VREQQPLSSLSSVLLYRSAPEDLRLLFYDEVSRLESFWALRVVCQEQLTALLAWIREPWE
 ELFSIGLRTVIQEALALDR

Figure 4.

- 63 -

>gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC33104.1|
 (AF082516) I-1 receptor candidate protein [Homo sapiens]
 Length = 1504

5 Score = 68.3 bits (164), Expect = 4e-10
 Identities = 69/256 (26%), Positives = 102/256 (38%), Gaps = 26/256 (10%)

Query: 107 VLQKTLCLKLVHVAGP-GPTG-----PIKIFPFKSLRHLELRGVPLHCLHGLRGIY 156
 +L T LK + V+G GP G P + FKSL +E+ + GL

10 Sbjct: 180 ILDFTCRLKYLKVSGETGPFPGTSNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASK 239

Query: 157 SQLETLICRSRLQALEELL-----SACGGDFCSALP-WLALLSANFSYNXX 201
 L TL S +++E+L + G + +P W AL + + S+N

Sbjct: 240 PTLATLSVRFSATSMKEVLVPEASEFDEWEPEGTTLEGPVTAVIPTWQALTTLDLSHNSI 299

15 Query: 202 XXXXXXXXXXXXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGAALG 261
 HN + L L L HLD+SYN+L + + +

Sbjct: 300 SEIDESVKLIPKIEFLDLSHNGLLVVDN-LQHLYNLVHLDLSYNKLSSLEGLHTKLGNIK 358

20 Query: 262 VLILRGNELRSLHGLEQLRNLRLHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHP 321
 L L GN L SL GL +L +L +LDL N +E E+ + L L + L NPL P

Sbjct: 359 TLNLAGNLLSLSGLHKLYSLVNLDLRDNRIEQMEEVRSIGSLPCLEHVSLNNPLSIIP 418

25 Query: 322 EHRAATAQYLSPRARD 337

++R RA +

Sbjct: 419 DYRTKVLAQFGERASE 434

Figure 5.

- 64 -

101 TACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC 2150
 ||||||||||||||||||||||||||||||||||||||||
 1644 TACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCCAGGATGGGATTAGAC 1693
 5
 2151 AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAG..... 2183
 ||||||||||||||||||||||||||||||||||||
 1694 AGTGAGGAAGGCTGGAGGCCTCTGTTCCAAAAGACAGAATCTCCTGCTGT 1743
 10
 2184ACAGGGAGCGGAAACAGGGAGAGCAGTCTCTGGCTCCTTCT 2224
 ||||||||||||||||||||||||||||||||||||
 15 1794 GAACCCCAACAGGGAGCGGAAACAGGGAGAGCAGTCTCTGGCTCCTTCT 1843
 2225 CCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACCTTGA 2274
 ||||||||||||||||||||||||||||||||||||
 20 1844 CCGTTTGCCAGCCCTGTCTGCCACCCTCCTGGCCATGGTGACCACCTTGA 1893
 2825 TCATCCTTGAGGCTCGCCAGTTCTTCTACCTTCGGGCGTTCCTGGTTGA 2874
 ||||||||||||||||||||||||||||||||||||
 2444 TCATCCTTGAGGCTCGCCAGTTCTTCTACCTTCGGGCGTTCCTGGTTGA 2493
 3375 ATCTGGGCCCCCTCCATGACCTTCCACACTGGATGCCTCTTCCCTGCAGG 3424
 ||||
 2494AGG 2496
 3425 CCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCGTCCACCCTGTTCC 3474
 ||||||||||||||||||||||||||||||||||||
 40 2497 CCCTTCCACCTGCCTCGTATCCCTGTTGCTGACTCCGTCCACCCTGTTCC 2546

Figure 6.

- 65 -

Query= sequence
(1114 letters)

Database: newnr
228,478 sequences; 162,186,938 total letters

Searching.....done

10 Sequences producing significant alignments:

	Score (bits)	E Value
gb AAF52305.1 (AE003611) CG9044 gene product [Drosophila melano...	127	5e-28
gi 6005788 imidazoline receptor candidate >gi 3462807 gb AAC3310...	68	4e-10
gb AAF57514.1 (AE003794) CG8595 gene product [Drosophila melano...	47	0.001

15 >gb|AAF52305.1| (AE003611) CG9044 gene product [Drosophila melanogaster]
Length = 1289

20 Score = 127 bits (317), Expect = 5e-28
Identities = 99/321 (30%), Positives = 149/321 (45%), Gaps = 11/321 (3%)

Query: 38 KLAGLLRESGDVVXXXXXXXXXXXXXXXXXNHVF-----ELHLGPWGPQGTFVALPSH 91
+LA LLR++GD + N F E+ G F +

Sbjct: 8 ELANLLRQNGDKILSSEFTLTLSGSLLRALNDSFTLIADTEIGTGAGYLQPSQSFQVVKPI 67

Query: 92 PADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP-TGPIKIFPFKSLRHLELRGVPLHCLH 150
A S V LQ + D +QKT LKL + G I I F++LR LE+ + + +

Sbjct: 68 NAKSSVFPDLQLVHDFVQKTTLLKLTYPSEHYFEGAIDIAKFRALRRLEVNKINIGQVV 127

Query: 151 GLRGIYSQLETLICSRSLQALEELLSACGGDFCSALPWLALLSANFSYNXXXXXXXXXXXXX 210
G++ + QL+ LIC +SL ++++++ CGGD + W L +A+FSYN

Sbjct: 128 GIQPLRGQLQHLCVKSLSVDDIITRCGGDNSNGFVWNEKLTADFSYNSLRSDTALEF 187

Query: 211 XXXXXXXXXXXXHNQVQDCQGFMDLCELHHLDISYNRLHLVPRMGPSGA-ALGVLIIRGNE 269
HN++ + L L LD+SYN L +P+ L +L + N

Sbjct: 188 AQHLQHLNLRHNKLTSAVA- IKWLPHLKTLDSLNCCLTHLPQFHMEACKRLQLLNISNNY 246

Query: 270 LRSLHGLEQLRNLRLHLDLAYNLLEGHRELSPLWLLAELRKLYLEGNPLWFHPEHRAATAQ 329
+ L + +L L +LDL+ N L H +L PL L L L L+GNPL +P+HR ATAQ

Sbjct: 247 VEELLDVAKLDALYNLDLSDNCLLEHSQLLPLSALMSLIVLNLQGNPLACNPKHRQATAQ 306

Query: 330 YLSPRARDAATGFLLDGKVLS 350
YL A F+LD + L+

Sbjct: 307 YL--HKNSATVKFVLDFFEPLT 325

Figure 7A

- 66 -

Score = 41.4 bits (95), Expect = 0.054

Identities = 41/151 (27%), Positives = 62/151 (40%), Gaps = 20/151 (13%)

5 Query: 814 VDHRLRLFLDVEVFSDAQEEFQCCLKVPVALAGHTGEFMCLVVVSDRRLYLLKVTGEMRE 873
 +DHRL+L+ F + E F+ K + LVV+S+ + YL++ E +
 Sbjct: 1018 IDHRLKLYFYQRKFEDGEHFKWLAKGRIYNEQTQSLGEGLVVMSNCKCYLMEAFAPHD 1077

10 Query: 874 PPASWLQLTLAVPLQDLSGIELGLAGQSLRLEWAAGA-----GRCVLLPRDARHCRAF 926
 A WL+ ++V + L I+L L W G G VLL D
 Sbjct: 1078 DVAKWLRQVVSVAVNRLVAIDL-----LPWKLGLSFTLKDGGFVLLLDHMLR---- 1125

Query: 927 LEELLDVLQSLPPAWRNCVSATEEEVTPQHR 957
 E LL+ LQ +P C + VT H+
 15 Sbjct: 1126 TESLLNYLQQIPLP-EQCKLNHQPSVTLSHQ 1155

>gi|6005788 imidazoline receptor candidate >gi|3462807|gb|AAC33104.1|
 (AF082516) I-1 receptor candidate protein [Homo sapiens]
 Length = 1504

Score = 68.3 bits (164), Expect = 4e-10

Identities = 69/256 (26%), Positives = 102/256 (38%), Gaps = 26/256 (10%)

Query: 107 VLQKTLSLKLHVHAGP-GPTG-----PIKIFPFKSLRHLELRGVPLHCLHGLRGIY 156
 +L T LK + V+G GP G P + FKSL +E+ + GL
 Sbjct: 180 ILDFTCRLKYLKVSGETGPFGTSTNIQEQLLPFDLSIFKSLHQVEISHCDAKHIRGLVASK 239

Query: 157 SQLETLICSRSLQALEELL-----SACGGDFCSALP-WLALLSANFSYNXX 201
 L TL S +++E+L + G + +P W AL + + S+N
 Sbjct: 240 PTLATLSVRFSATSMKEVLVPEASEFDEWEPEGTTLEGPVTAIPTWQALTTLDLSHNSI 299

Query: 202 XXXXXXXXXXXXXXXXXXXXHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGAALG 261
 HN + L L L HLD+SYN+L + + +
 Sbjct: 300 SEIDESVKLIPKIEFLDLSHNGLLVVDN-LQHLYNLVHLDLSYNKLSSLEGLHTKLGNIK 358

Query: 262 VLILRGNELRSLHGLEQLRNLRLHLDLAYNLLLEGHRELSPLWLLAELRKLYLEGNPLWFHP 321
 L L GN L SL GL +L +L +LDL N +E E+ + L L + L NPL P
 Sbjct: 359 TLNLAGNLLLESGLHKLYSLVNLDLRDNRIEQMEEVRSIGSLPCLEHVSLLNNPLSIIP 418

Query: 322 EHRAATAQYLSPRARD 337
 ++R RA +
 Sbjct: 419 DYRTKVLAQFGERASE 434

Figure 7B

- 67 -

5 FL1-18_SPLICE_VARIANT
 FL1-18
 Drosophila_melanogaster_CG9044
 imidazoline_receptor_candidate
 ---MFGSAPQRPVAMTTAQRDS---LLWKLAGLLRESGD-----
 ---MFGSAPQRPVAMTTAQRDS---LLWKLAGLLRESGD-----
 -----MDPQK-----ITELANLLRQNGD-----
 MATARTFGPEREAPAKEARVVGSELVDYTVYIIQVTDGSHEWTVKHRY
 *:: : : : *

10 FL1-18_SPLICE_VARIANT
 FL1-18
 Drosophila_melanogaster_CG9044
 imidazoline_receptor_candidate
 -----VVLSCGCTLSLLTP-----
 -----VVLSCGCTLSLLTP-----
 -----KILSSEFTLTLSGS-----
 SDFHDLHEKLVARERKIDKNLLPPKKIIGKNSRSLVEKREKDLEVYLQKLL
 : . . * .

15 FL1-18_SPLICE_VARIANT
 FL1-18
 Drosophila_melanogaster_CG9044
 imidazoline_receptor_candidate
 -----TLQQLNHVFELHLG-----PWG
 -----TLQQLNHVFELHLG-----PWG
 -----LLRALNDSFTLIADT-----EIG
 AAFPVGVTFRVLAHFLHFHYEINGITAALAEELFEKGEQLLGAGEVFAIG
 : * . : : *

20 FL1-18_SPLICE_VARIANT
 FL1-18
 Drosophila_melanogaster_CG9044
 imidazoline_receptor_candidate
 PG---Q-TGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP
 PG---Q-TGFVALPSHPADSPVILQLQFLFDVLQKTLSLKLVHVAGPGP
 TGAGYLQPSQFQVVKPINAKSSVFPDLQLVHDFVQKTTLLKLTYPSEHY
 PLQLYAVTEQLQQGKPTCASGDAKDLGHILDFTCRLKYLKVSGETGPGF
 : . . * . . : * : * : * :

25 FL1-18_SPLICE_VARIANT
 FL1-18
 Drosophila_melanogaster_CG9044
 imidazoline_receptor_candidate
 -----TGPIKIFPFKSLRHLELRGVPLHCHLGLRGIYSQLETLICSR
 -----TGPIKIFPFKSLRHLELRGVPLHCHLGLRGIYSQLETLICSR
 F-----EGAIIDIAKFRALRRLEVKNINIGQVVGIQPLRQLQHLICVKS
 TSNIEQLLFPDLISIFKSLHQVEISHCAKHIRGLVASKPTLATLSVRS
 : : : * : : : : : : : * : * : *

30 FL1-18_SPLICE_VARIANT
 FL1-18
 Drosophila_melanogaster_CG9044
 imidazoline_receptor_candidate
 LQALEELLSACGGDFCSALP-----WLALLSANFSYNALT
 LQALEELLSACGGDFCSALP-----WLALLSANFSYNALT
 LTSVDDIITRCGGDNSNGFV-----WNEKLTADFSYNLSR
 ATSMKEVLVPEASEFEDEWEPEGTTLEGPVTAIPTWQALTTLDLSHNSIS
 : : : : : . . * * : : : * : :

35 FL1-18_SPLICE_VARIANT
 FL1-18
 Drosophila_melanogaster_CG9044
 imidazoline_receptor_candidate
 ALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPR
 ALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPR
 SVDTALEFAQHLQHLNLRHNKLTSA-AIKWLPKLTLDLSYNCLTHLPQ
 EIDESVKLI PKIEFLDLSHNGLLVVD-NLQHLNVLVHLDLSYNKLSLEG
 : * : : : : . . * * : : * * * : * :

40 FL1-18_SPLICE_VARIANT
 FL1-18
 Drosophila_melanogaster_CG9044
 imidazoline_receptor_candidate
 -MGPSGAALGVLIILRGNELRSLHGLEQLRNLRLHLDLAYNLLEGHRELSPL
 -MGPSGAALGVLIILRGNELRSLHGLEQLRNLRLHLDLAYNLLEGHRELSPL
 FHMEACKRLQLLNISNNYVEELLDVAKLDALYNLDLSDNCLLEHSQLLPL
 -LHTKLGNIKTNLNLAGNLLSLSGLHKLKLYSLVNLDRDNRIEQMEEVRSI
 : * : * : . . * : : * * : * : : :

50 FL1-18_SPLICE_VARIANT
 FL1-18
 Drosophila_melanogaster_CG9044
 imidazoline_receptor_candidate
 WLLAELRKLYLEGNPLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSL
 WLLAELRKLYLEGNPLWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSL
 SALMSLIVLNLQGNPLACNPKHRQATAQYLYHKN--ATVKFVLDFEPLTK
 GSLPCLEHVSLLNPLSIIPDYRTKVLAQFGERA----SEVCLDDTVTTE
 * * : * . * * * * : * : : : * * :

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Figure 8A

Figure 8B

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-----VLLYRSAPEDLRLLFYD-----EV-----S
-----LSNLVDVERITDQKYAINFID-----ET-----Q
RDLDRVLMGYQTYPQALTLVFDDVQGHDLMGSVTLDFHGEVPGGPARASQ

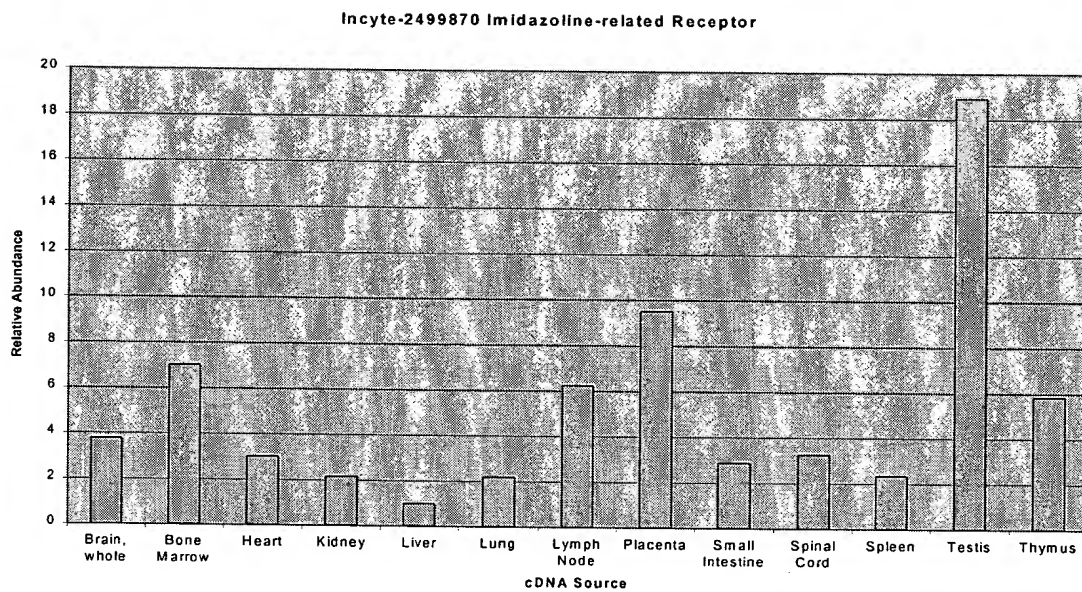
RLSEFWALRVVCQEQLTALLAWIREPWEEFISIGLRTVIQEALALDR

NRCEIWKLFQETHANAACCLNVIGKGWEQLFGVPFSLSGT-----
GREVQWQVFVPSAESREKLISLLARQWEALCGRELPVELTG-----

(* REPRESENTS RESIDUES THAT ARE IDENTICAL IN ALL FOUR PRTEINS; : REPRESENTS RESIDUES THAT ARE OF SIMILAR BIOCHEMICAL CHARACTER IN 3 OUT OF THE 4 PROTEINS; . REPRESENTS RESIDUES THAT ARE OF SIMILAR BIOCHEMICAL CAHARACTER IN 2 OUT OF THE 4 PROTEINS).

Figure 8D

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**Figure 9.**

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FL1 - Imidazoline Receptor

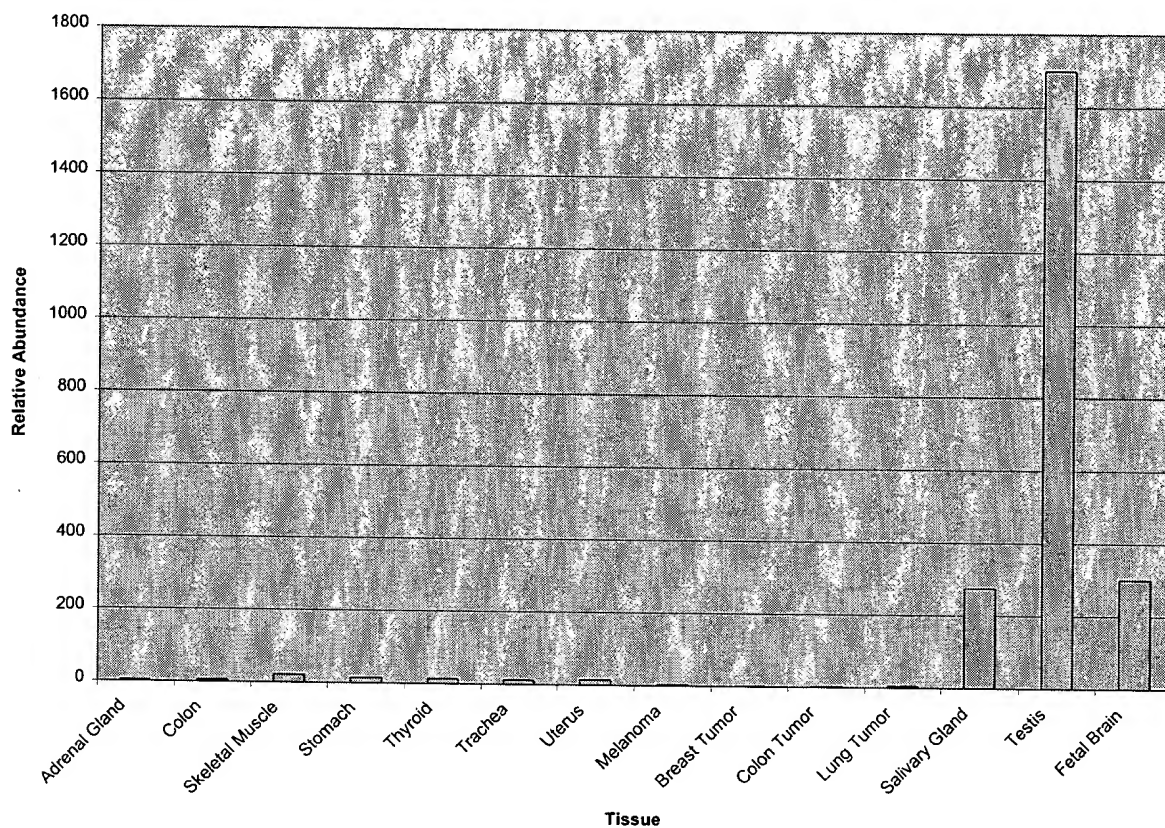


Figure 10.